# Modeling COVID-19 pandemic using Bayesian analysis with application to Slovene data - Supplementary Material 1

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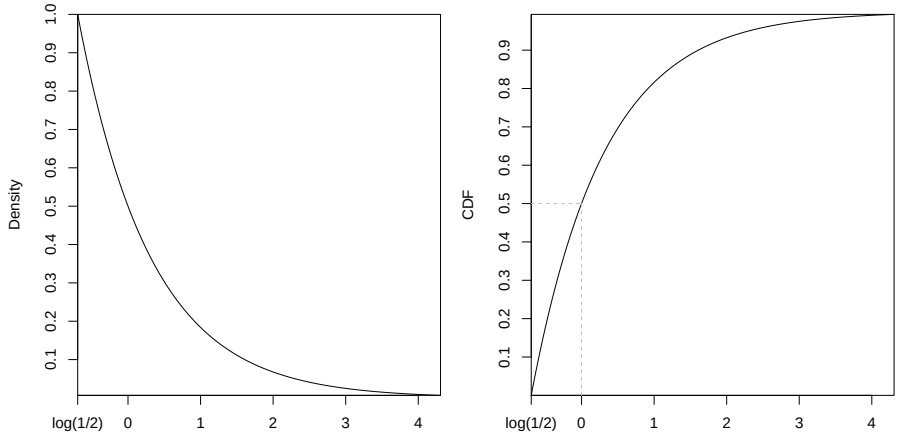
## S1 Details on the prior for $\alpha_k$

Here we show the density and cumulative distribution function (CDF) of the prior for parameters $\alpha_k$, see Figure S1.

Figure S1: Density and cumulative distribution function (CDF) of the prior for parameters $\alpha_k$.



# S2 Sensitivity analysis for the choice of the prior distributions for positive quantities

We performed a sensitivity analysis replacing the folded-normal distribution that is used in the main model with other commonly used prior distributions for positive quantities, i.e. gamma and log-normal distributions. With $X \sim \text{Lognormal}(\mu, \sigma)$ we denote a log-normal distribution for which $\log(X)$ is normally distributed with mean $\mu$ and standard deviation $\sigma$. Two types of analyses were performed. In the first analysis, all folded-normal priors (except for $\phi^{\mathcal{X}}$ which remained unchanged) were replaced with log-normal or gamma priors with equal mean and variance as used in the folded-normal prior (see Table S1). In the second analysis, the priors for $\phi^{\mathcal{X}}$ were additionally replaced by log-normal and gamma priors where the priors chosen for $\phi^{\mathcal{X}}$ were

$$\text{Lognormal}\left(\log(\psi^{\mathcal{X}} \cdot \frac{2}{\pi}), \sqrt{log(\frac{\pi}{2})}\right)$$

when using log-normal priors and

$$\Gamma\left(\sqrt{\frac{2}{\pi}}\psi^{\mathcal{X}}, \sqrt{\frac{\pi}{2} - 1}\right),$$

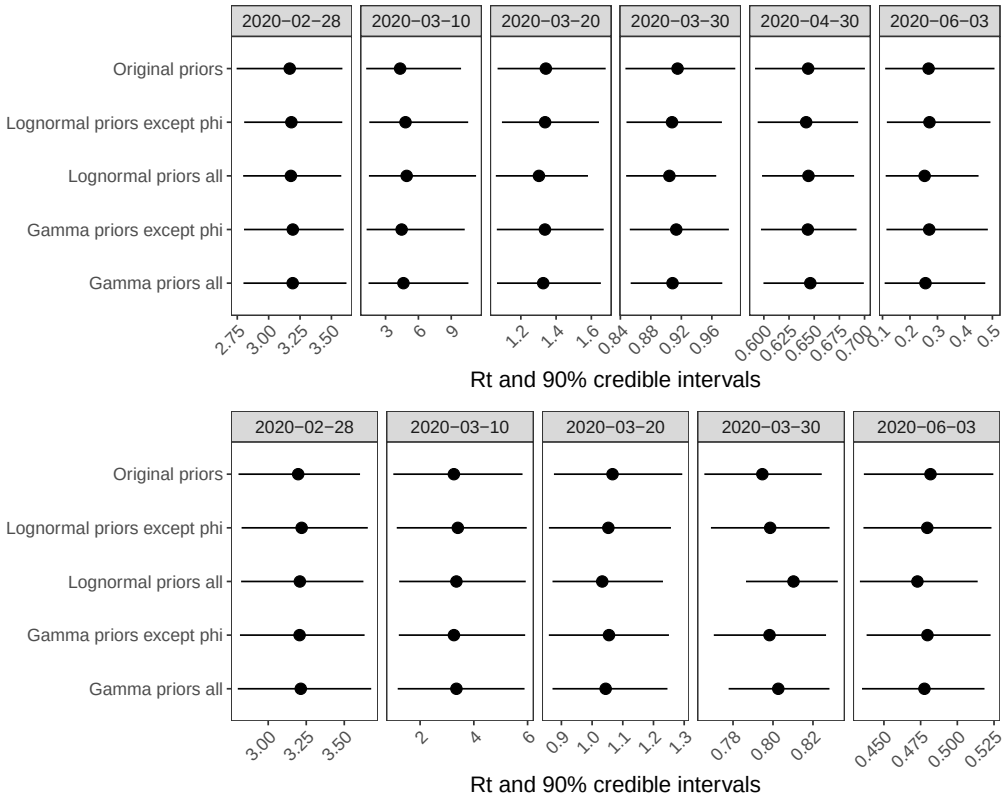
when using gamma priors. These priors were used so that the mean and variance are the same as in the original analysis.

Table S1: Prior distributions for positive quantities.

| Parameters | Original model | Gamma | Log-normal |
|---|---|---|---|
| $\phi^{\mathcal{X}}$ | $\mathcal{N}^+(0, \psi^{\mathcal{X}})$ | $\mathcal{N}^+(0, \psi^{\mathcal{X}})$ | $\mathcal{N}^+(0, \psi^{\mathcal{X}})$ |
| $\psi^{\mathcal{X}}$ | $\mathcal{N}^+(8, 2)$ | $\Gamma(8.001, 0.25)$ | Lognormal(2.049,0.246) |
| $\eta^{\mathcal{X}}$ | $\mathcal{N}^+(1, 0.5)$ | $\Gamma(1.009, 0.479)$ | Lognormal(-0.095,0.454) |
| $R_0$ | $\mathcal{N}^+(3.28, 0.25)$ | $\Gamma(3.28, 0.076)$ | Lognormal(1.185, 0.076) |

Figure S2 shows estimates of the reproduction number at different dates (point estimates with 90% CI) for different choices of the prior distributions. We can see that the estimates are very similar.

Figure S2: Reproduction number estimates for the different models at given dates. The first column gives the basic reproduction number, and the others are the reproduction number estimates at different dates of major government interventions corresponding to $G_1 < G_2 < G_3 < G_4$ and the final date. The reproduction number is modeled using natural splines (upper panel) and piece-wise constant function (lower panel).



# S3 Sensitivity analysis for modeling over-dispersion

We performed a sensitivity analysis for the $\phi^{\mathcal{X}}$ parameters choosing less informative priors:

$$\psi^{\mathcal{X}} \sim \mathcal{N}^{+}(8, 10) \text{ or } \psi^{\mathcal{X}} \sim \mathcal{N}^{+}(8, 100).$$

As an alternative way of modelling over-dispersion, we also considered a frequently used approach where the model is re-parameterized such that

$$X_t \sim \text{NegBin}\left(x_t, x_t + \left(x_t \phi^{\mathcal{X}}\right)^2\right),$$

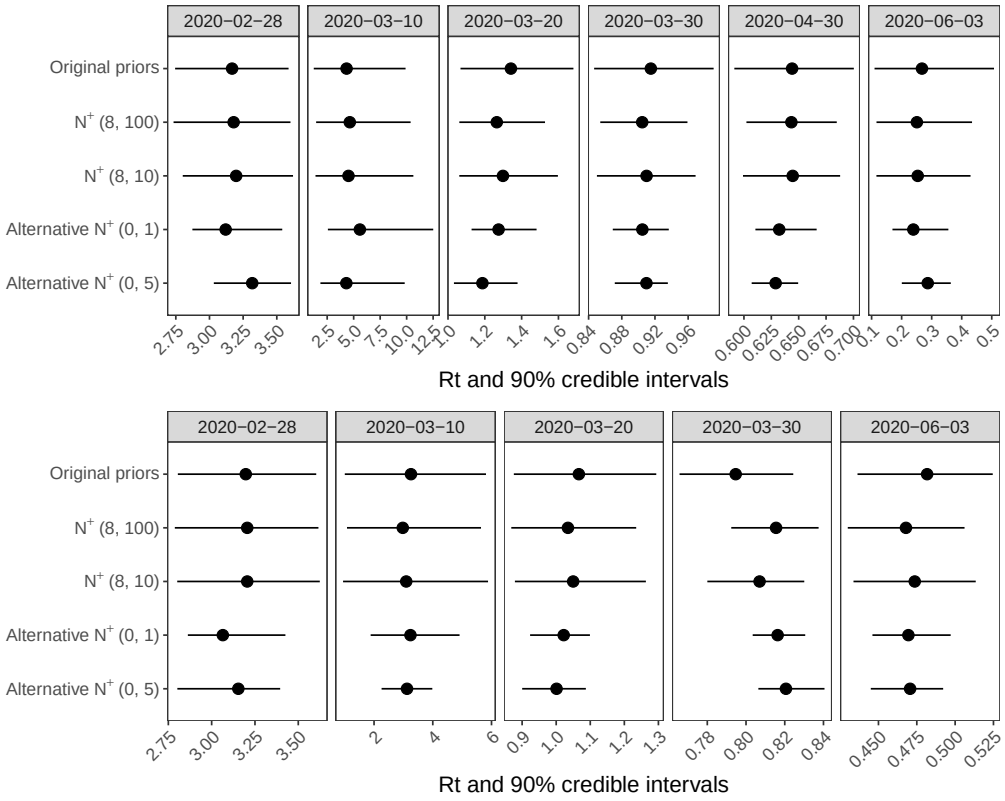
where

$$\phi^{\mathcal{X}} \sim \mathcal{N}^{+}(0, 1) \text{ or } \phi^{\mathcal{X}} \sim \mathcal{N}^{+}(0, 5).$$

This re-parametrization allows for no over-dispersion.

Figure S3 shows estimates of the reproduction number at different dates (point estimates with 90% CI) for different choices of the prior distributions. It can be seen that similar results are obtained for different choices of the prior distributions for the over-dispersion parameters.

Figure S3: Reproduction number estimates for the different models at given dates. The first column given the basic reproduction number, and the others are the reproduction number estimates at different dates of major government interventions corresponding to $G_1 < G_2 < G_3 < G_4$ and the final date. The reproduction number is modeled using natural splines (upper panel) and piece-wise constant function (lower panel).



# S4 Comparison with the Flaxman model

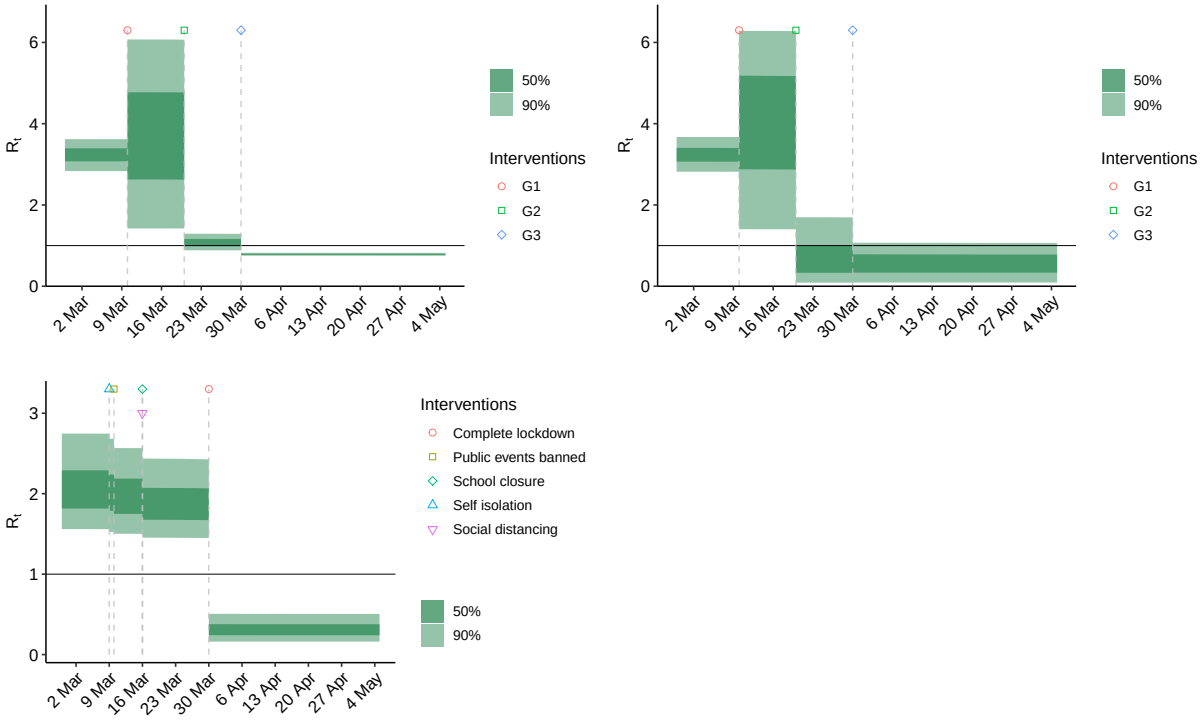
Here we compare the model presented in Section 2.1 in the main text with the model proposed by Flaxman et al. and evaluate the effect of including several data sources in our model. For comparability with the Flaxman model, Slovene data at the national level up to and including May 5, 2020, considering $G_1 < G_2 < G_3$ in our proposed approach using a piece-wise constant function to model $R_t$ were considered.

In the Flaxman model, additionally to the data for 11 countries as used in [1], data on daily number of deaths for Slovenia were added in the analysis, specifying the following dates for the NPIs: 1) self-isolation (March 9, 2020), 2) public event banned (March 10, 2020), 3) school closure (March 16, 2020), 4) social distancing encouraged (March 16, 2020) and 5) complete lock-down (March 30, 2020), see [1] for more details. Note that close spacing of interventions in time means that in the Flaxman model the individual effects of the interventions prior to the last one are not identifiable [1], therefore tempering the comparison between our and Flaxman model prior to March 30, 2020 (i.e. $G_3$).

For evaluating the effect of including several data sources in our proposal, we consider the model where only the data on the daily number of deaths are included in our model. In this case, $c_t$ are only informed by $D_t$: in Figure 1 only the *branch* to $d_t^C$ remains and $d_t^C$, $D_t^C$, $\mu^{\mathcal{D}^C}$, $\xi^{\mathcal{D}^C}$ and $\tau^{\mathcal{D}^C}$ are replaced by all deaths, $d_t$, $D_t$, $\mu^{\mathcal{D}}$, $\xi^{\mathcal{D}}$ and $\tau^{\mathcal{D}}$, respectively. We used $\mu^{\mathcal{D}} = 18.8$, $\xi^{\mathcal{D}} = 0.45$ and $\tau^{\mathcal{D}} = 0.00954$ as in [2].

In Figure S4 we show $R_t$ for our proposed approach (top left), the approach using only data on daily number of deaths (top right), and for the Flaxman model (bottom left). Comparing the results after the last intervention (March 30, 2020), it can be seen in Figure S4 that using all available data sources results in much narrower CIs than when only using the data on the daily number of deaths. Using the Flaxman model results, after the last intervention, in slightly wider CIs and also smaller estimates of $R_t$ than when using our proposed approach with all available data. The latter is a consequence of pooling information from other countries where the effects of interventions were larger than in Slovenia.

Figure S4: Estimated $R_t$ for our proposed approach (top left), the approach using only data on daily number of deaths (top right), and for the Flaxman model (bottom left) using Slovene data for the period from 28-2-2020 to 5-5-2020 and piece-wise constant function when modeling $R_t$.



# References

[1] S. Flaxman, S. Mishra, A. Gandy, H. Unwin, T. Mellan, H. Coupland, C. Whittaker, H. Zhu, T. Berah, J. Eaton, M. Monod, A. Ghani, C. Donnelly, S. Riley, M. Vollmer, N. Ferguson, L. Okell, S. Bhatt, P. Perez-Guzman, P. Walker, Estimating the effects of non-pharmaceutical interventions on covid-19 in europe, Nature 584 (2020) 257–261. doi:10.1038/s41586-020-2405-7.

[2] D. Manevski, M. Pohar Perme, R. Blagus, Estimation of the reproductive number and the outbreak size of sars-cov-2 in slovenia, Slovenian Medical Journal 89 (2020) 1–12. doi:10.6016/ZdravVestn.3068.
URL `https://vestnik.szd.si/index.php/ZdravVest/article/view/3068`